EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20030224353"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:48
L2	2703	sars or hsars or hcov	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:49
L3	396	full adj genom$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:53
L4	4	2 with 3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:49
L5	13706	full with genom$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:50
L6	8	2 with 5 not 4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:50
L7	16	hku-39849 or hku adj "39849" or hku39849	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:56
L8	0	hku-39 or hku adj "39" or hku39	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/06/23 14:56

```
? ds

Set     Items   Description
S1      12902   CORONAVIR? OR CORONA(W)VIR?
S2      12936   CORONAVIR? OR CORONA(W)(VIRUS OR VIRUSES OR VIRAL)
S3      67616   CONSENSUS
S4         96   S3 AND S2
S5      33626   UNIVERSAL
S6    1318082   DETECT?
S7         38   S2 AND S6 AND (S3 OR S5)
S8   18643642   PY<2003
S9         20   S7 AND S8
S10      4726   SARS
S11        13   S7 AND S10
? log hold
       23jun06 09:32:46 User208669 Session D3044.3
            $0.13    0.039 DialUnits File155
     $0.13  Estimated cost File155
            $0.18    0.039 DialUnits File50
     $0.18  Estimated cost File50
            $0.88    0.039 DialUnits File357
     $0.88  Estimated cost File357
            OneSearch, 3 files,  0.118 DialUnits FileOS
     $0.02  TELNET
     $1.21  Estimated cost this search
     $1.21  Estimated total session cost   0.118 DialUnits
Logoff: level 05.12.03 D  09:32:46
```

```
=> d his

     (FILE 'HOME' ENTERED AT 08:31:59 ON 23 JUN 2006)

     FILE 'REGISTRY' ENTERED AT 08:32:07 ON 23 JUN 2006
L1             0 S (GGGACTATCCTAAGTGTGA OR TAACACACAACICCATCATCA)/SQN
L2            38 S (GGGACTATCCTAAGTGTGA OR TAACACACAACICCATCATCA)/SQSN
L3             0 S L1 AND SQL<100

     FILE 'CA' ENTERED AT 08:33:46 ON 23 JUN 2006
L4            26 S L2
L5            11 S L4 AND SARS
L6            15 S L4 NOT SARS
L7            11 S L4 AND PRIMER?
L8             2 S L4 AND CONSENSUS

=> log hold
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      42.74     105.93

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                         ENTRY    SESSION
CA SUBSCRIBER PRICE                                      -1.42      -1.42

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 08:36:09 ON 23 JUN 2006
```

NCBI megablast BLAST

Nucleotide | Protein | Translations | Retrieve results for an RID

What is Mega BLAST?

Search
```
atattaggtttttacctacccaggaaaagccaaccaacctcgatctcttgtagatctgtt
ctctaaacgaactttaaaatctgtgtagctgtcgctcggctgcatgcctagtgcacctac
gcagtataaacaataataaattttactgtcgttgacaagaaacgagtaactcgtccctct
tctgcagactgcttacggtttcgtccgtgttgcagtcgatcatcagcatacctaggtttc
gtccgggtgtgaccgaaaggtaagatggagagccttgttcttggtgtcaacgagaaaaca
```

Load query file from disk: Browse...

Set subsequence: From: To:

Choose database: nr

Return alignment endpoints only: ☐

Now: BLAST! or

Options for advanced blasting

Limit by entrez query: or select from: All organisms

Choose filter: ☑ Low complexity ☐ Human repeats ☐ Mask for lookup table only ☐ Mask lower case

Expect: 10

Word Size: 28

Percent Identity, match, mismatch scores: None, 1, -2

Other advanced:

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi Alignment in HTML format

☐ CDS feature

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

NCBI

formatting BLAST

Nucleotide | Protein | Translations | Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (29,742 letters)

The request ID is 1151085824-31454-204534673121.BLASTQ4

Format! or Cancel

The results are estimated to be ready in 10 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi Alignment in HTML format

☐ CDS feature

Masking Character Lower Case Masking Color Grey

Number of: Descriptions 100 Alignments 50 Graphic overview 100

Alignment view Hit Table

Start formatting from query #

Limit results by entrez query or select from: All organisms

Expect value range:

Results file ☐

NCBI *results of* BLAST

```
# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: nr
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q. star
# 50 hits found
```

1_31454	gi|30023963|gb|AY278491.2|	100.00	29727	0	0	1	29727	1
1_31454	gi|33115118|gb|AY323977.2|	99.97	29728	8	2	1	29727	1
1_31454	gi|30698326|gb|AY291451.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|40548933|gb|AY502928.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|40548897|gb|AY502925.1|	99.97	29728	8	2	1	29727	1
1_31454	gi|52546959|gb|AY714217.1|	99.96	29728	9	2	1	29727	1
1_31454	gi|30248028|gb|AY274119.3|	99.96	29728	9	2	1	29727	1
1_31454	gi|31873092|gb|AY321118.1|	99.96	29728	7	3	1	29727	1
1_31454	gi|40548921|gb|AY502927.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548909|gb|AY502926.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548945|gb|AY502929.1|	99.96	29728	10	2	1	29727	1
1_31454	gi|33518725|gb|AY362699.1|	99.96	29728	10	2	1	29727	1
1_31454	gi|40548969|gb|AY502931.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|40548957|gb|AY502930.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|33518724|gb|AY362698.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|33411399|dbj|AP006557.1|	99.96	29728	11	2	1	29727	1
1_31454	gi|30027617|gb|AY278741.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|31581502|gb|AY291315.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|33578015|gb|AY310120.1|	99.95	29728	12	2	1	29727	1
1_31454	gi|40548981|gb|AY502932.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|37576845|gb|AY427439.1|	99.97	29712	7	2	17	29727	1
1_31454	gi|38505491|gb|AY485278.1|	99.95	29728	10	4	1	29727	1
1_31454	gi|40548873|gb|AY502923.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|37624341|gb|AY394998.1|	99.97	29713	8	2	16	29727	1
1_31454	gi|33411459|dbj|AP006561.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|33411444|dbj|AP006560.1|	99.95	29728	13	2	1	29727	1
1_31454	gi|67003761|gb|AY864805.1|	99.95	29728	14	2	1	29727	1
1_31454	gi|38304867|gb|AY282752.2|	99.96	29713	9	2	16	29727	1
1_31454	gi|33411429|dbj|AP006559.1|	99.95	29728	14	2	1	29727	1
1_31454	gi|38231927|gb|AY350750.1|	99.96	29715	10	2	14	29727	1
1_31454	gi|30468042|gb|AY283794.1|	99.96	29712	9	2	17	29727	1
1_31454	gi|30468044|gb|AY283796.1|	99.96	29712	9	2	17	29727	1
1_31454	gi|33114202|gb|AY345987.1|	99.96	29713	10	2	16	29727	1
1_31454	gi|33114190|gb|AY345986.1|	99.96	29713	10	2	16	29727	1
1_31454	gi|33411414|dbj|AP006558.1|	99.94	29728	13	4	1	29727	1
1_31454	gi|38231932|gb|AY357075.1|	99.96	29714	9	4	15	29727	1
1_31454	gi|37361915|gb|AY283798.2|	99.96	29712	11	2	17	29727	1
1_31454	gi|38505482|gb|AY485277.1|	99.94	29728	13	3	1	29727	1
1_31454	gi|67003775|gb|AY864806.1|	99.94	29728	17	2	1	29727	1
1_31454	gi|37624333|gb|AY394990.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|37624332|gb|AY394989.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|33114214|gb|AY345988.1|	99.95	29713	12	2	16	29727	1
1_31454	gi|45644994|gb|AY559081.1|	99.95	29713	11	3	17	29727	4
1_31454	gi|45645004|gb|AY559087.1|	99.94	29712	16	2	17	29727	1
1_31454	gi|37624334|gb|AY394991.1|	99.95	29713	13	2	16	29727	1
1_31454	gi|45645007|gb|AY559088.1|	99.95	29714	12	4	17	29727	1
1_31454	gi|99078934|gb|DQ497008.1|	99.93	29728	20	2	1	29727	1
1_31454	gi|37624336|gb|AY394993.1|	99.95	29713	14	2	16	29727	1
1_31454	gi|37624335|gb|AY394992.1|	99.95	29713	14	2	16	29727	1
1_31454	gi|45645023|gb|AY559096.1|	99.95	29709	13	2	20	29727	12

NCBI *nucleotide-nucleotide* BLAST

Nucleotide | Protein | Translations | Retrieve results for an RID

Search
```
atattaggtttttacctacccaggaaaagccaaccaacctcgatctcttgtagatctgtt
ctctaaacgaactttaaaatctgtgtagctgtcgctcggctgcatgcctagtgcacctac
gcagtataaacaataataaattttactgtcgttgacaagaaacgagtaactcgtccctct
tctgcagactgcttacggtttcgtccgtgttgcagtcgatcatcagcatacctaggtttc
gtccgggtgtgaccgaaaggtaagatggagagccttgttcttggtgtcaacgagaaaaca
```

Set subsequence From: To:

Choose database nr

Now: BLAST! or Put results in Batch

Options for advanced blasting

Limit by entrez query or select from: All organisms

Choose filter ☑ Low complexity ☐ Human repeats ☐ Mask for lookup table only ☐ Mask lower case

Expect 10

Word Size 11

Other advanced

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi Alignment in HTML format

☐ CDS feature

Masking Character Lower Case Masking Color Grey

Number of: Descriptions 100 Alignments 50 Graphic overview 100

Alignment view Pairwise

Limit results by entrez query or select from: All organisms

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

NCBI

Nucleotide Protein Translations formatting BLAST Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (29,742 letters)

The request ID is 1151086129-31006-68807045580.BLASTQ4

Format! or Manage

The results are estimated to be ready in 14 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☑ Graphical Overview ☑ Linkout ☑ Sequence Retrieval ☑ NCBI-gi Alignment in HTML format

☐ CDS feature

Masking Character Lower Case Masking Color Grey

Number of: Descriptions 100 Alignments 50 Graphic overview 100

Alignment view Pairwise

Limit results by entrez query or select from: All organisms

Expect value range:

NCBI results of BLAST

BLASTN 2.2.14 [May-07-2006]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1151086129-31006-68807045580.BLASTQ4

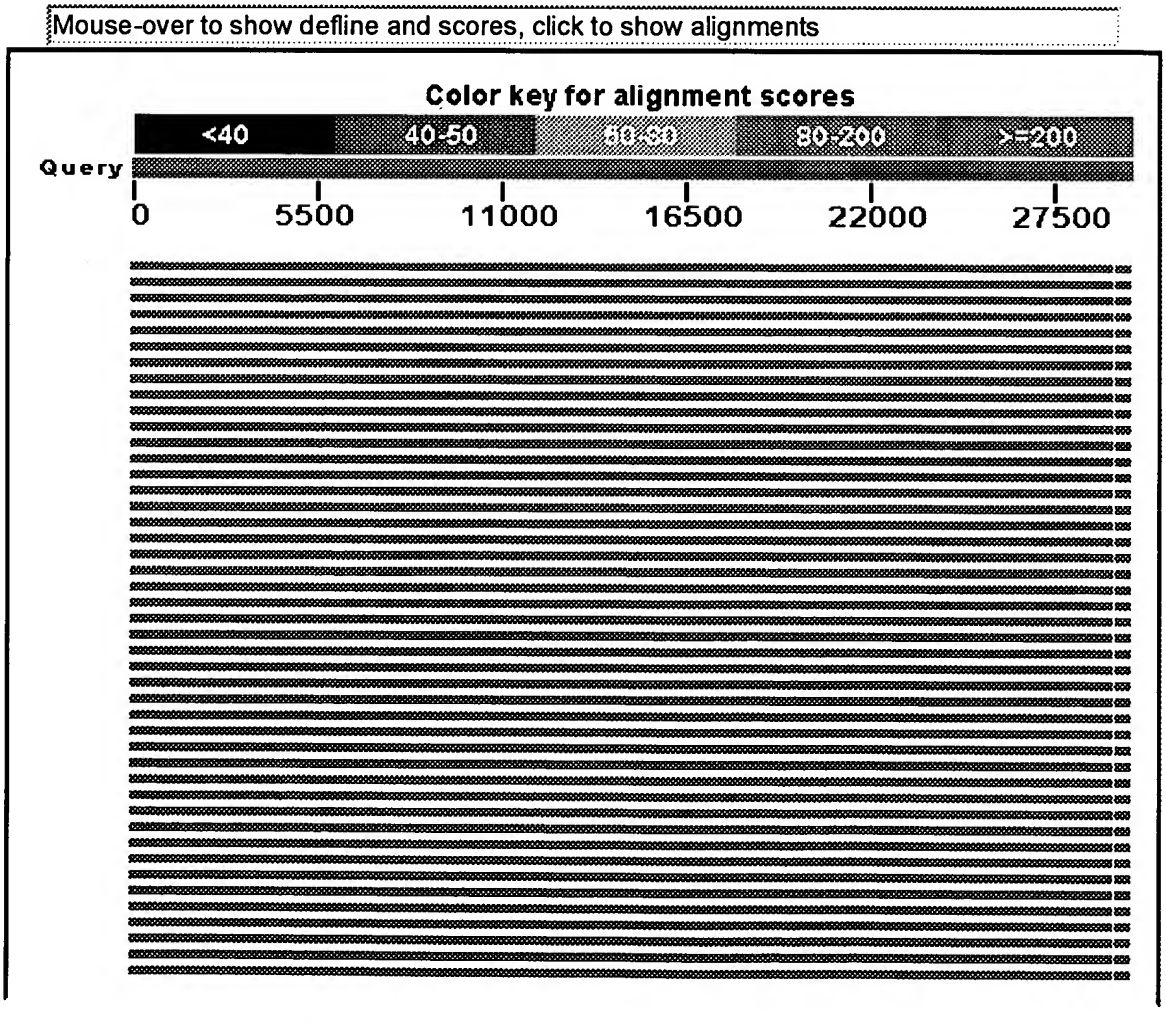
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
4,084,561 sequences; 17,475,977,371 total letters

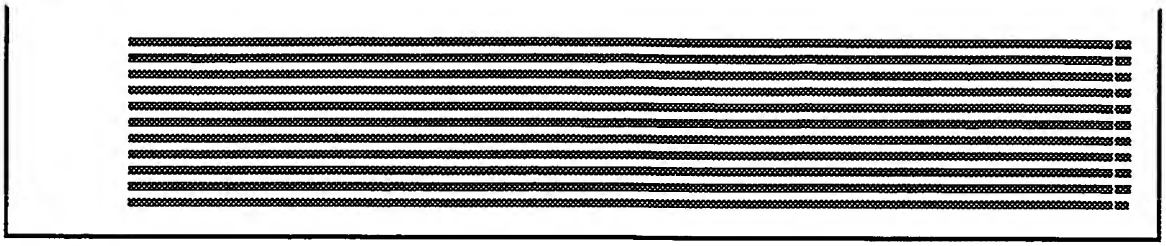
If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Query=
Length=29742

Distribution of 226 Blast Hits on the Query Sequence





Distance tree of results NEW

Sequences producing significant alignments:		Score (Bits)	E Value
gi|30023963|gb|AY278491.2|	SARS coronavirus HKU-39849, complete	5.785e+04	0.0
gi|33115118|gb|AY323977.2|	SARS coronavirus HSR 1, complete geno	5.777e+04	0.0
gi|30698326|gb|AY291451.1|	SARS coronavirus TW1, complete genome	5.777e+04	0.0
gi|40548933|gb|AY502928.1|	SARS coronavirus TW5, complete genome	5.777e+04	0.0
gi|40548897|gb|AY502925.1|	SARS coronavirus TW2, complete genome	5.777e+04	0.0
gi|52546959|gb|AY714217.1|	SARS Coronavirus CDC#200301157, compl	5.776e+04	0.0
gi|30248028|gb|AY274119.3|	SARS coronavirus TOR2, complete genom	5.776e+04	0.0
gi|31873092|gb|AY321118.1|	SARS coronavirus TWC, complete genome	5.775e+04	0.0
gi|40548945|gb|AY502929.1|	SARS coronavirus TW6, complete genome	5.775e+04	0.0
gi|40548921|gb|AY502927.1|	SARS coronavirus TW4, complete genome	5.775e+04	0.0
gi|40548909|gb|AY502926.1|	SARS coronavirus TW3, complete genome	5.775e+04	0.0
gi|33518725|gb|AY362699.1|	SARS coronavirus TWC3, complete genom	5.775e+04	0.0
gi|40548969|gb|AY502931.1|	SARS coronavirus TW8, complete genome	5.775e+04	0.0
gi|40548957|gb|AY502930.1|	SARS coronavirus TW7, complete genome	5.774e+04	0.0
gi|37576845|gb|AY427439.1|	SARS coronavirus AS, complete genome	5.774e+04	0.0
gi|33518724|gb|AY362698.1|	SARS coronavirus TWC2, complete genom	5.774e+04	0.0
gi|33411399|dbj|AP006557.1|	SARS coronavirus TWH genomic RNA, co	5.774e+04	0.0
gi|37624341|gb|AY394998.1|	SARS coronavirus LC1, complete genome	5.774e+04	0.0
gi|30027617|gb|AY278741.1|	SARS coronavirus Urbani, complete gen	5.774e+04	0.0
gi|31581502|gb|AY291315.1|	SARS coronavirus Frankfurt 1, complet	5.774e+04	0.0
gi|33578015|gb|AY310120.1|	SARS coronavirus FRA, complete genome	5.774e+04	0.0
gi|40548981|gb|AY502932.1|	SARS coronavirus TW9, complete genome	5.773e+04	0.0
gi|38304867|gb|AY282752.2|	SARS coronavirus CUHK-Su10, complete	5.773e+04	0.0
gi|38505491|gb|AY485278.1|	SARS coronavirus Sino3-11, complete g	5.773e+04	0.0
gi|40548873|gb|AY502923.1|	SARS coronavirus TW10, complete genom	5.773e+04	0.0
gi|30468042|gb|AY283794.1|	SARS coronavirus Sin2500, complete ge	5.773e+04	0.0
gi|30468044|gb|AY283796.1|	SARS coronavirus Sin2679, complete ge	5.773e+04	0.0
gi|33411459|dbj|AP006561.1|	SARS coronavirus TWY genomic RNA, co	5.773e+04	0.0
gi|33411444|dbj|AP006560.1|	SARS coronavirus TWS genomic RNA, co	5.773e+04	0.0
gi|38231927|gb|AY350750.1|	SARS coronavirus PUMC01, complete gen	5.773e+04	0.0
gi|33114202|gb|AY345987.1|	SARS coronavirus CUHK-AG02, complete	5.772e+04	0.0
gi|33114190|gb|AY345986.1|	SARS coronavirus CUHK-AG01, complete	5.772e+04	0.0
gi|67003761|gb|AY864805.1|	SARS coronavirus BJ162, complete geno	5.772e+04	0.0
gi|33411429|dbj|AP006559.1|	SARS coronavirus TWK genomic RNA, co	5.772e+04	0.0
gi|37361915|gb|AY283798.2|	SARS coronavirus Sin2774, complete ge	5.771e+04	0.0
gi|38231932|gb|AY357075.1|	SARS coronavirus PUMC02, complete gen	5.771e+04	0.0
gi|37624333|gb|AY394990.1|	SARS coronavirus HZS2-E, complete gen	5.771e+04	0.0
gi|37624332|gb|AY394989.1|	SARS coronavirus HZS2-D, complete gen	5.771e+04	0.0
gi|33114214|gb|AY345988.1|	SARS coronavirus CUHK-AG03, complete	5.771e+04	0.0
gi|33411414|dbj|AP006558.1|	SARS coronavirus TWJ genomic RNA, co	5.771e+04	0.0
gi|38505482|gb|AY485277.1|	SARS coronavirus Sino1-11, complete g	5.770e+04	0.0
gi|45644994|gb|AY559081.1|	SARS coronavirus Sin842, complete gen	5.770e+04	0.0
gi|37624334|gb|AY394991.1|	SARS coronavirus HZS2-Fc, complete ge	5.770e+04	0.0
gi|67003775|gb|AY864806.1|	SARS coronavirus BJ202, complete geno	5.770e+04	0.0
gi|45645004|gb|AY559087.1|	SARS coronavirus Sin3725V, complete g	5.769e+04	0.0
gi|45645023|gb|AY559096.1|	SARS coronavirus Sin850, complete gen	5.769e+04	0.0
gi|37624336|gb|AY394993.1|	SARS coronavirus HGZ8L2, complete gen	5.769e+04	0.0
gi|37624335|gb|AY394992.1|	SARS coronavirus HZS2-C, complete gen	5.769e+04	0.0
gi|30468045|gb|AY283797.1|	SARS coronavirus Sin2748, complete ge	5.769e+04	0.0
gi|38231937|gb|AY357076.1|	SARS coronavirus PUMC03, complete gen	5.769e+04	0.0

gi|45645007|gb|AY559088.1|	SARS coronavirus SinP1, complete geno	5.768e+04	0.0
gi|99078934|gb|DQ497008.1|	SARS coronavirus strain MA-15, comple	5.768e+04	0.0
gi|74275570|gb|DQ182595.1|	SARS coronavirus ZJ0301 from China, c	5.768e+04	0.0
gi|45645017|gb|AY559092.1|	SARS coronavirus SinP5, complete geno	5.768e+04	0.0
gi|40548885|gb|AY502924.1|	SARS coronavirus TW11, complete genom	5.768e+04	0.0
gi|38385714|gb|AY461660.1|	SARS coronavirus SoD, complete genome	5.768e+04	0.0
gi|30468043|gb|AY283795.1|	SARS coronavirus Sin2677, complete ge	5.768e+04	0.0
gi|30027610|gb|AY278554.2|	SARS coronavirus CUHK-W1, complete ge	5.768e+04	0.0
gi|45645000|gb|AY559084.1|	SARS coronavirus Sin3765V, complete g	5.767e+04	0.0
gi|45645022|gb|AY559095.1|	SARS coronavirus Sin847, complete gen	5.767e+04	0.0
gi|34482146|gb|AY304495.1|	SARS coronavirus GZ50, complete genom	5.767e+04	0.0
gi|45645019|gb|AY559093.1|	SARS coronavirus Sin845, complete gen	5.767e+04	0.0
gi|45645016|gb|AY559091.1|	SARS coronavirus SinP4, complete geno	5.766e+04	0.0
gi|45645001|gb|AY559085.1|	SARS coronavirus Sin848, complete gen	5.766e+04	0.0
gi|37624330|gb|AY394987.1|	SARS coronavirus HZS2-Fb, complete ge	5.765e+04	0.0
gi|40795428|gb|AY394850.2|	SARS coronavirus WHU, complete genome	5.765e+04	0.0
gi|50365700|gb|AY654624.1|	SARS coronavirus TJF, complete genome	5.765e+04	0.0
gi|30275666|gb|AY278488.2|	SARS coronavirus BJ01, complete genom	5.764e+04	0.0
gi|37624326|gb|AY394983.1|	SARS coronavirus HSZ2-A, complete gen	5.764e+04	0.0
gi|40795744|gb|AY508724.1|	SARS coronavirus NS-1, complete genom	5.763e+04	0.0
gi|31416306|gb|AY279354.2|	SARS coronavirus BJ04, complete genom	5.763e+04	0.0
gi|31416292|gb|AY278487.3|	SARS coronavirus BJ02, complete genom	5.761e+04	0.0
gi|32493129|gb|AY338174.1|	SARS coronavirus Taiwan TC1, complete	5.761e+04	0.0
gi|31416305|gb|AY278490.3|	SARS coronavirus BJ03, complete genom	5.759e+04	0.0
gi|33188324|gb|AY348314.1|	SARS coronavirus Taiwan TC3, complete	5.758e+04	0.0
gi|32493130|gb|AY338175.1|	SARS coronavirus Taiwan TC2, complete	5.757e+04	0.0
gi|108597802|gb|DQ640652.1|	SARS coronavirus GDH-BJH01, complete	5.756e+04	0.0
gi|45645013|gb|AY559090.1|	SARS coronavirus SinP3, complete geno	5.756e+04	0.0
gi|49176846|gb|AY595412.1|	SARS coronavirus LLJ-2004, complete g	5.755e+04	0.0
gi|45645010|gb|AY559089.1|	SARS coronavirus SinP2, complete geno	5.720e+04	0.0
gi|37624337|gb|AY394994.1|	SARS coronavirus HSZ-Bc, complete gen	5.498e+04	0.0
gi|37624338|gb|AY394995.1|	SARS coronavirus HSZ-Cc, complete gen	5.496e+04	0.0
gi|37624329|gb|AY394986.1|	SARS coronavirus HSZ-Cb, complete gen	5.489e+04	0.0
gi|45644996|gb|AY559082.1|	SARS coronavirus Sin852, complete gen	5.484e+04	0.0
gi|41323719|gb|AY390556.1|	SARS coronavirus GZ02, complete genom	5.484e+04	0.0
gi|45644998|gb|AY559083.1|	SARS coronavirus Sin3408, complete ge	5.482e+04	0.0
gi|45645003|gb|AY559086.1|	SARS coronavirus Sin849, complete gen	5.481e+04	0.0
gi|37624340|gb|AY394997.1|	SARS coronavirus ZS-A, complete genom	5.476e+04	0.0
gi|37624339|gb|AY394996.1|	SARS coronavirus ZS-B, complete genom	5.476e+04	0.0
gi|37624344|gb|AY395001.1|	SARS coronavirus LC4, complete genome	5.473e+04	0.0
gi|37624343|gb|AY395000.1|	SARS coronavirus LC3, complete genome	5.473e+04	0.0
gi|37624345|gb|AY395002.1|	SARS coronavirus LC5, complete genome	5.473e+04	0.0
gi|37624342|gb|AY394999.1|	SARS coronavirus LC2, complete genome	5.473e+04	0.0
gi|37624321|gb|AY394978.1|	SARS coronavirus GZ-B, complete genom	5.472e+04	0.0
gi|34482137|gb|AY304486.1|	SARS coronavirus SZ3, complete genome	5.470e+04	0.0
gi|37624322|gb|AY394979.1|	SARS coronavirus GZ-C, complete genom	5.468e+04	0.0
gi|45645021|gb|AY559094.1|	SARS coronavirus Sin846, complete gen	5.459e+04	0.0
gi|92698732|dbj|AB257344.1|	SARS coronavirus Frankfurt 1 geno...	5.423e+04	0.0
gi|60267744|gb|AY772062.1|	SARS coronavirus WH20, complete genom	5.391e+04	0.0
gi|39980888|gb|AY286320.4|	SARS coronavirus ZJ01, partial genome	5.199e+04	0.0

Alignments

Get selected sequences | Select all | Deselect all | Tree View

> ☐ gi|30023963|gb|AY278491.2| SARS coronavirus HKU-39849, complete genome
Length=29742

Score = 5.785e+04 bits (29181), Expect = 0.0
Identities = 29226/29226 (100%), Gaps = 0/29226 (0%)
Strand=Plus/Plus

```
Query  1      ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT  60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1        ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT  60

Query  61       CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61       CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC  120

Query  121      GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121      GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT  180

Query  181      TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181      TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC  240

Query  241      GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241      GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA  300
```

```
? ds

Set     Items   Description
S1       3809   SARS
S2          0   PD>2004
S3    1532886   PY>2003
S4       2213   S1 AND S3
S5      88358   PUTATIVE
S6         33   S4 AND S5
? log hold
       23jun06 12:35:54 User208669 Session D3045.2
           $17.86    5.253 DialUnits File155
               $0.00  33 Type(s) in Format  6
               $2.42  11 Type(s) in Format  7
            $2.42  44 Types
    $20.28  Estimated cost File155
     $2.66  TELNET
    $22.94  Estimated cost this search
    $23.86  Estimated total session cost   5.511 DialUnits
Logoff: level 05.12.03 D  12:35:54
```